

09/67345

Systematic Gene Search in the Incyte LifeSeq Database

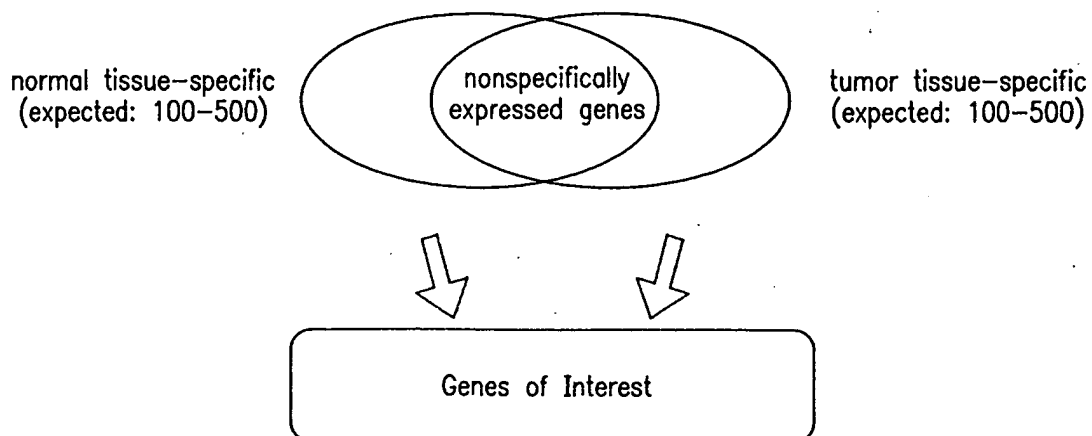
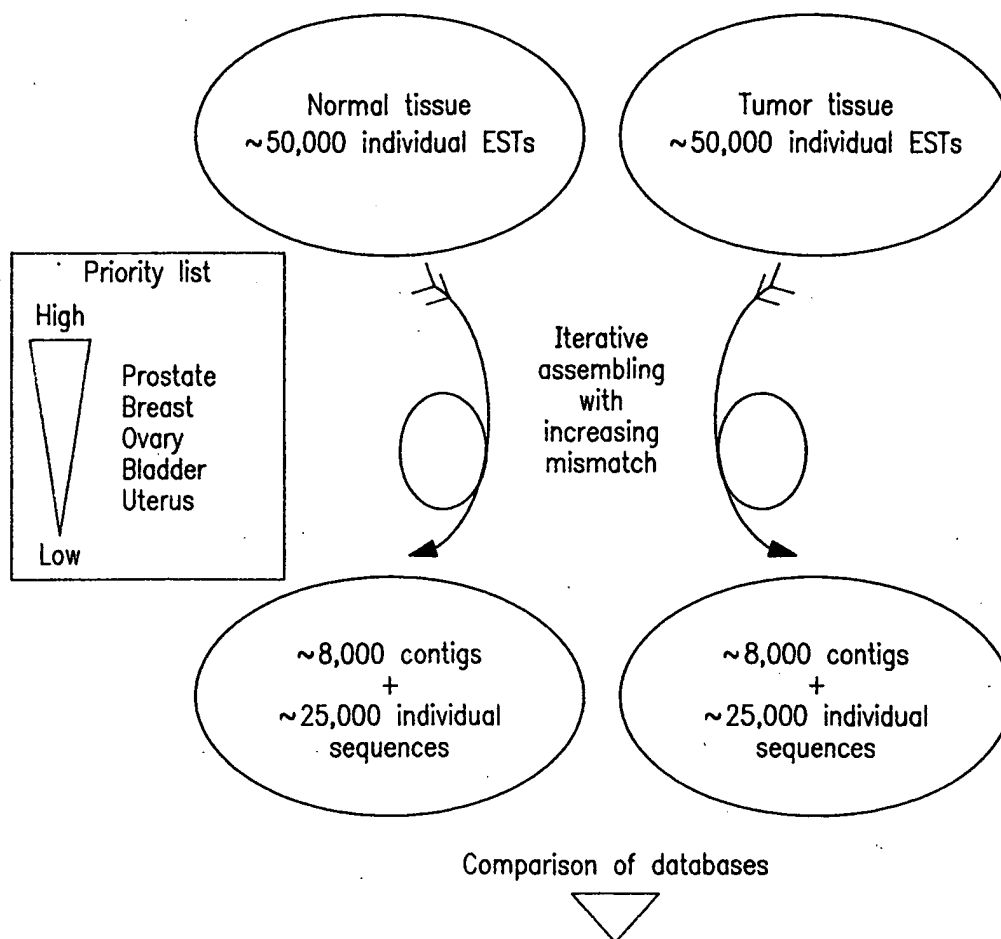


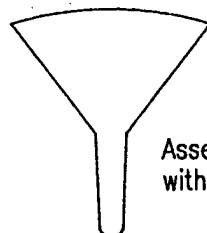
FIG. 1

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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Principle of EST Assembly

~50,000 ESTs per tissue



Assembly at 0% mismatch
with GAP4 (Staden)

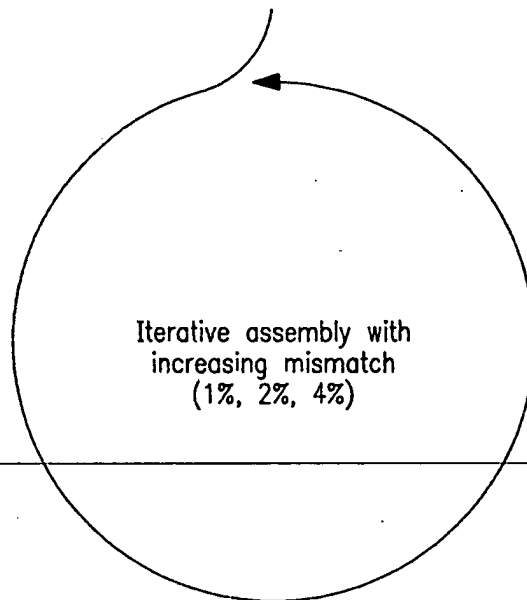


Contigs

Individual Sequences



Contigs increasing in
number and length



Iterative assembly with
increasing mismatch
(1%, 2%, 4%)

5000-6000 Contigs

~25,000 other individual
sequences



~30,000 consensus-
sequences per tissue

FIG. 2a

002231 0042960

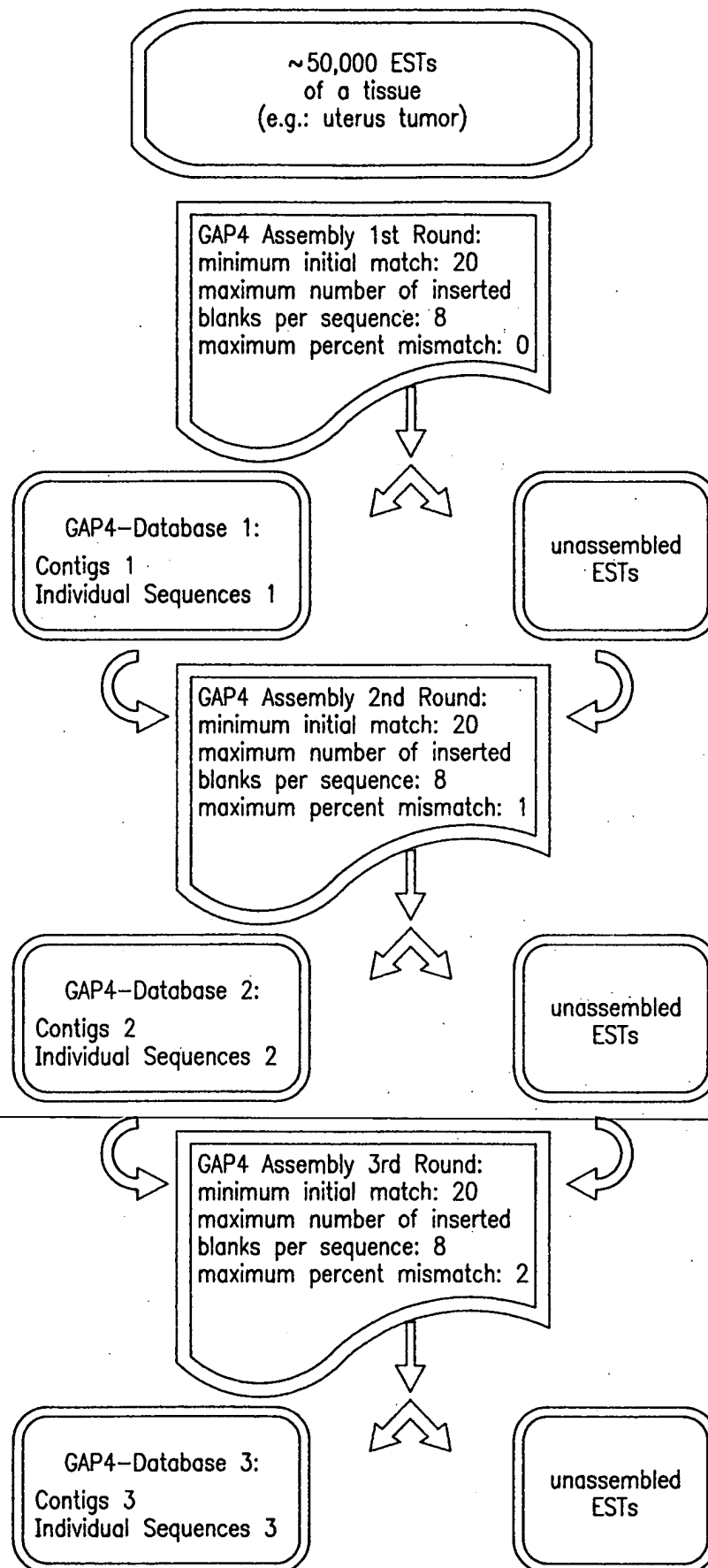


FIG. 2b-I

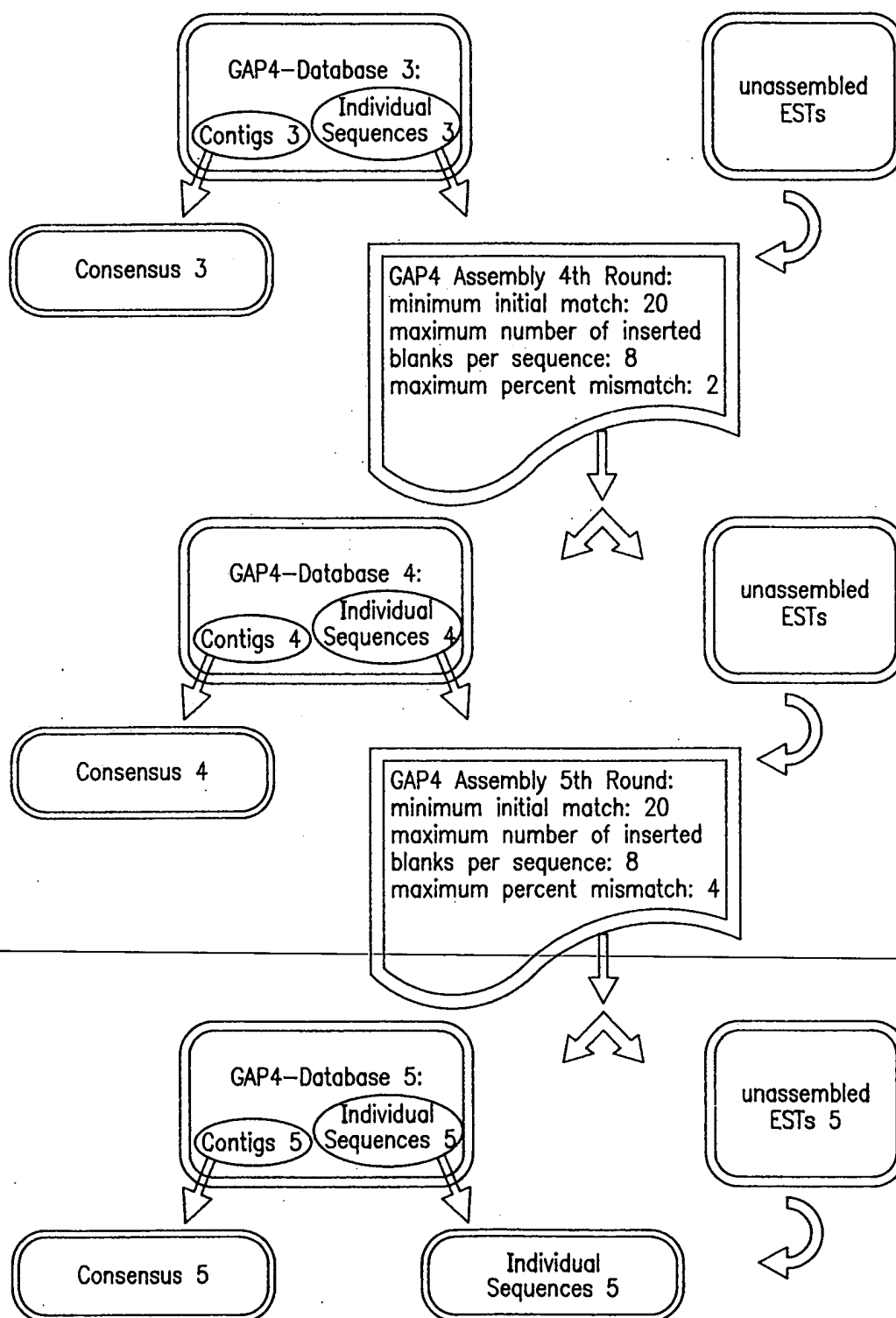


FIG. 2b-2

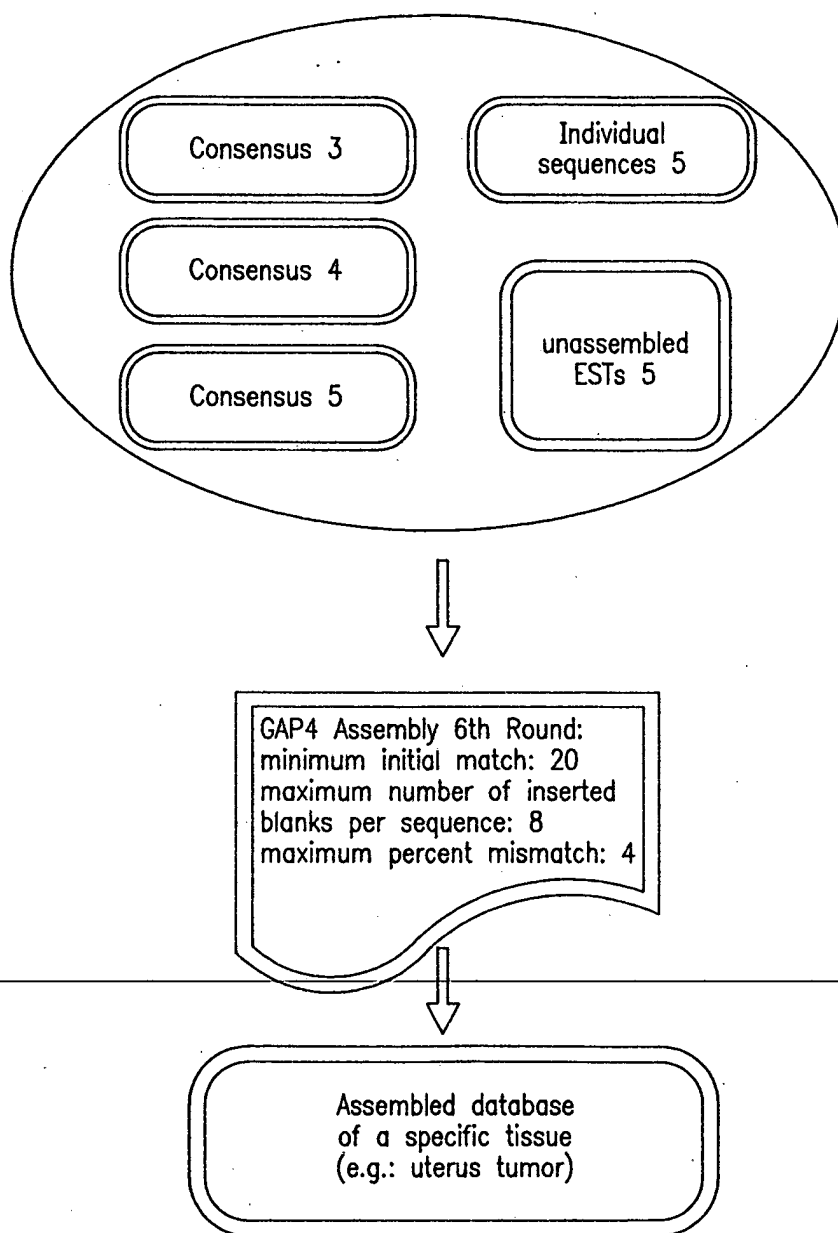


FIG. 2b-3

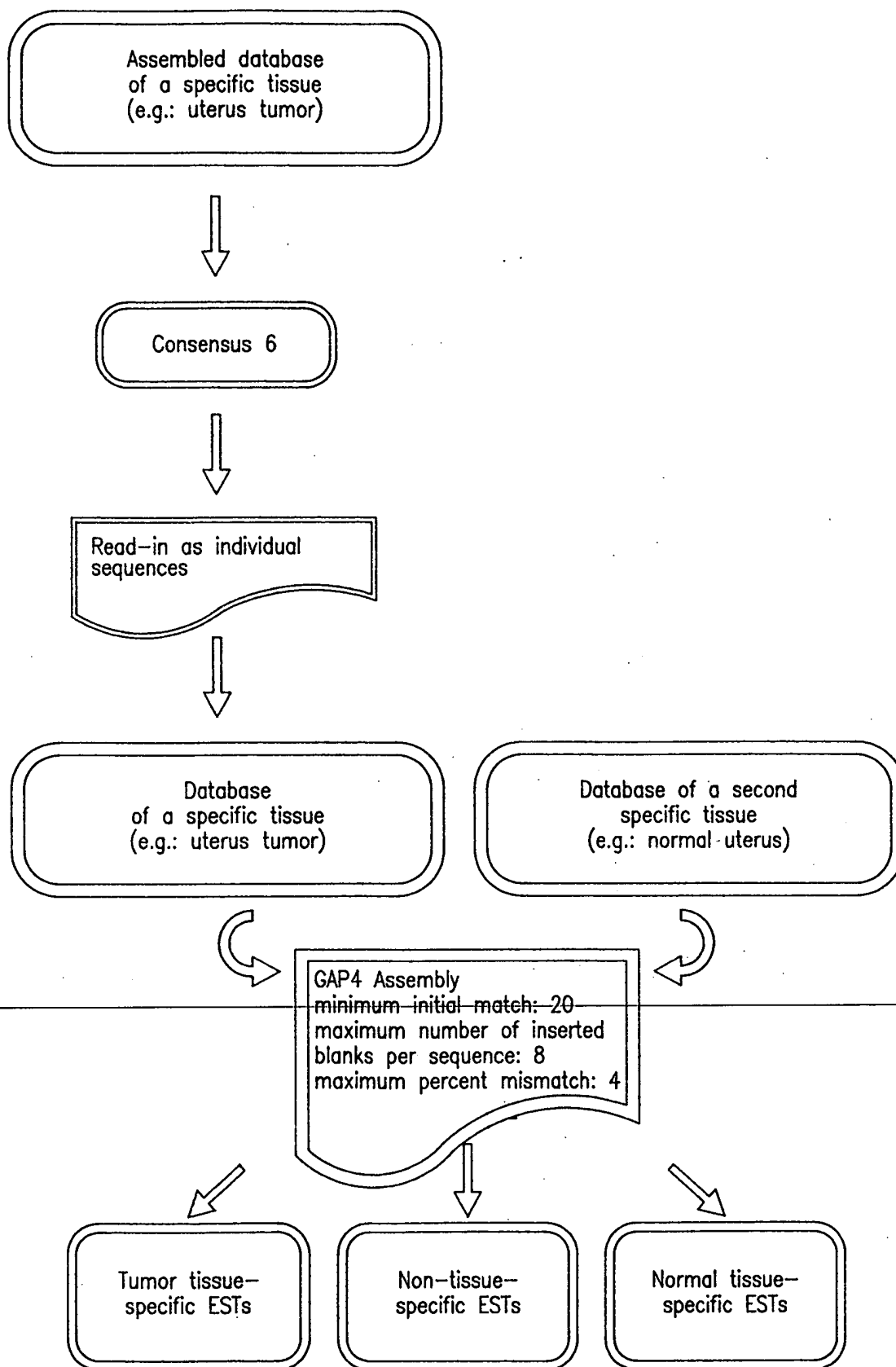
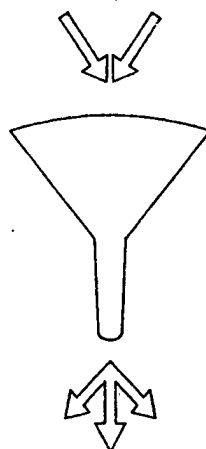


FIG. 2b-4

In silico subtraction of gene expression in various tissues

~30,000 consensus sequences
normal tissue

~30,000 consensus sequences
tumor tissue



Assembly at 4% mismatch

Normal tissue
Specific genes

Cancer tissue
Specific genes

Genes expressed in both tissues

FIG. 3

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004224 004224 004224

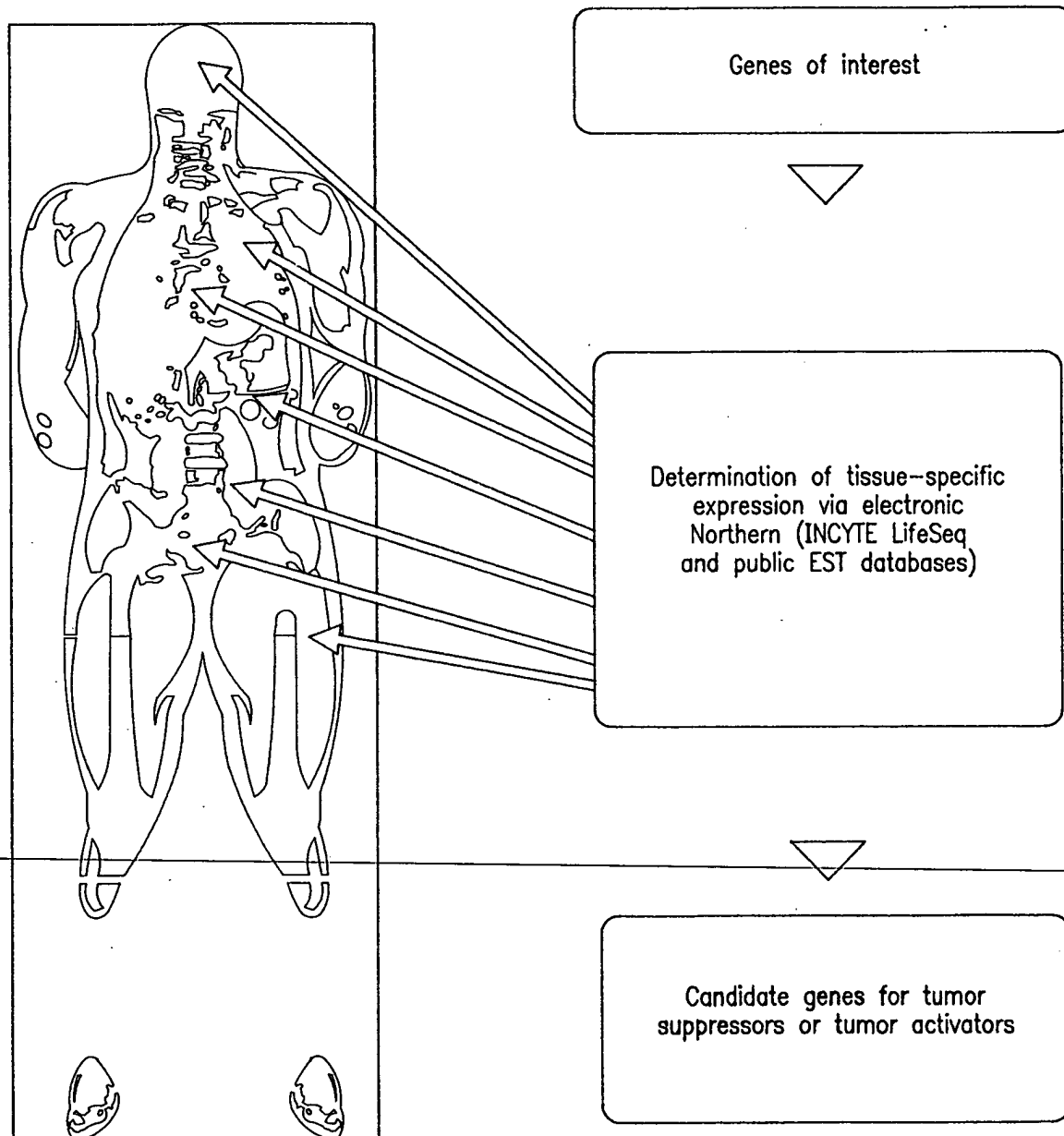


FIG. 4a

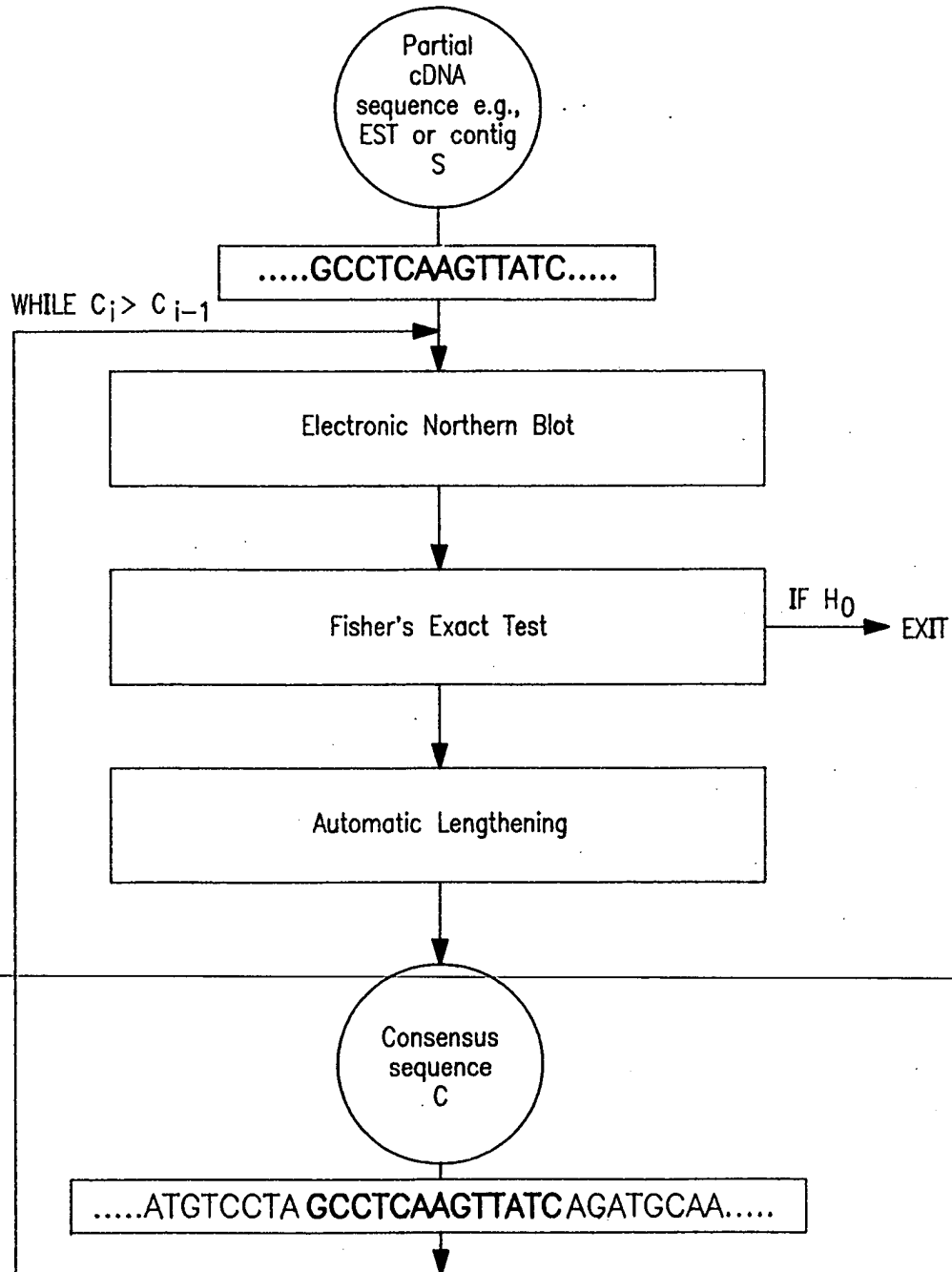


FIG. 4b

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09/673488-12200

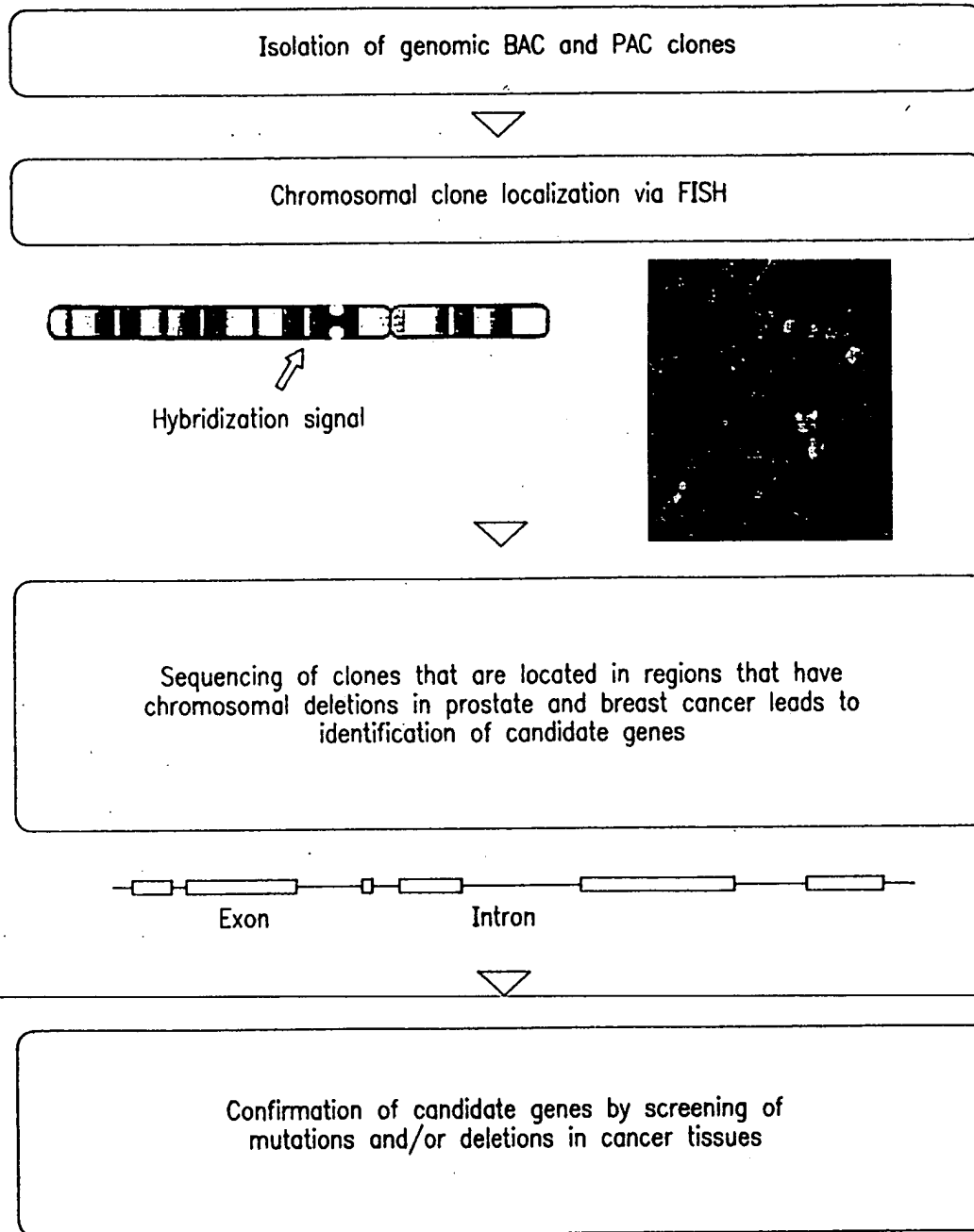


FIG. 5